C. Yaen

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RAW SEQUENCE LISTING              DATE: 09/15/2003
PATENT APPLICATION:  US/09/194,164    TIME: 15:42:28

Input Set : N:\Crf3\RULE60\09194164.RAW.txt
Output Set: N:\CRF4\09152003\I194164.raw
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SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Dan, Michael D.
 6                    Maiti, Pradip K.
 7                    Kaplan, Howard A.
 9     (ii) TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
10                    SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING
THE
11          '         FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
12                    DETECTION OF CANCERS
14    (iii) NUMBER OF SEQUENCES: 18
16     (iv) CORRESPONDENCE ADDRESS:
17          (A) ADDRESSEE: Morrison & Foerster
18          (B) STREET: 755 Page Mill Road
19          (C) CITY: Palo Alto
20          (D) STATE: CA
21          (E) COUNTRY: USA
22          (F) ZIP: 94304-1018
24      (v) COMPUTER READABLE FORM:
25          (A) MEDIUM TYPE: Floppy disk
26          (B) COMPUTER: IBM PC compatible
27          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30     (vi) CURRENT APPLICATION DATA:
C--> 31          (A) APPLICATION NUMBER: US/09/194,164
C--> 32          (B) FILING DATE: 09-Apr-1999
33          (C) CLASSIFICATION:
36    (vii) PRIOR APPLICATION DATA:
37          (A) APPLICATION NUMBER: US/08/657,449
38          (B) FILING DATE:
41   (viii) ATTORNEY/AGENT INFORMATION:
42          (A) NAME: Lehnhardt, Susan K.
43          (B) REGISTRATION NUMBER: 33,943
44          (C) REFERENCE/DOCKET NUMBER: 31608-20001.00
46     (ix) TELECOMMUNICATION INFORMATION:
47          (A) TELEPHONE: (415) 813-5600
48          (B) TELEFAX: (415) 494-0792
49          (C) TELEX: 706141
52 (2) INFORMATION FOR SEQ ID NO: 1:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 543 base pairs
56          (B) TYPE: nucleic acid
57          (C) STRANDEDNESS: double
58          (D) TOPOLOGY: linear
```

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62      (ix) FEATURE:
63           (A) NAME/KEY: CDS
64           (B) LOCATION: 1..543
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 CAAGCTATTT AGGTGACACT ATAGAATACT CAAGCTATGC ATCCAACGCG TTGGGAGCTC      60
71 TCCCATATGG TCGACCTGCA GGCGGCCGCA CTAGTGATTT CAAGCTTCAT CACTGAACAC     120
73 AGAGGACTCA CCATGGAGTT TGGGCTGAGC TGGGTTTTCC TCGTTGCTCT TTTAAGAGGT     180
75 ATCCAGTGTC AGGTGCAGCT GGTGGAGTCT GGGGGAGGCG TGGTCCAGCC TGGGAGGTCC     240
77 CTGAGACTCT CCTGTGCAGC CTCTGGATTC CCCTTCAGAA GCTTTGCTAT GCACTGGGTC     300
79 CGCCAGGCTC TAGGCAAGGG GCTGGAGTGG GTGGCAGTTA TATCATATGA TGGAAGCACT     360
81 AAATACTACG CAGACTCCGT GAAGGGGCGA TTCACCATCT CCAGAGACAC TTCCAAGAAC     420
83 ACGGTGTATC TAAAAATGAA CAGGCTGAGA ACTGAGGACA CGGCTGTCTT TTACTTGTGC     480
85 GAAAGACAGA GCCTGCTGGG TGACTATGAC CACTACTACG GNTTGGACGC TTGGGGAAAG     540
87 GGA                                                                  543
89 (2) INFORMATION FOR SEQ ID NO: 2:
91      (i) SEQUENCE CHARACTERISTICS:
92           (A) LENGTH: 179 amino acids
93           (B) TYPE: amino acid
94           (C) STRANDEDNESS: single
95           (D) TOPOLOGY: linear
101     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
103     Gln Ala Ile Val Thr Leu Asn Thr Gln Ala Met His Pro Thr Arg Trp
104     1               5                   10                  15
106     Glu Leu Ser His Met Val Asp Leu Gln Ala Ala Ala Leu Val Ile Ser
107                 20                  25                  30
109     Ser Phe Ile Thr Glu His Arg Gly Leu Thr Met Glu Phe Gly Leu Ser
110             35                  40                  45
112     Trp Val Phe Leu Val Ala Leu Leu Arg Gly Ile Gln Cys Gln Val Gln
113         50                  55                  60
115     Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
116     65                  70                  75                  80
118     Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Arg Ser Phe Ala Met His
119                 85                  90                  95
121     Trp Val Arg Gln Ala Leu Gly Lys Gly Leu Glu Trp Val Ala Val Ile
122                 100                 105                 110
124     Ser Tyr Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
125             115                 120                 125
127     Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Val Tyr Leu Lys Met
128         130                 135                 140
130     Asn Arg Leu Arg Thr Glu Asp Thr Ala Val Phe Tyr Leu Cys Glu Arg
131     145                 150                 155                 160
133     Gln Ser Leu Leu Gly Asp Tyr Asp His Tyr Tyr Gly Leu Asp Ala Trp
134                 165                 170                 175
136     Gly Lys Gly
139 (2) INFORMATION FOR SEQ ID NO: 3:
141     (i) SEQUENCE CHARACTERISTICS:
142           (A) LENGTH: 543 base pairs
143           (B) TYPE: nucleic acid
144           (C) STRANDEDNESS: double
```

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```
145              (D) TOPOLOGY: linear
151      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
153 TCCCTTTCCC CAAGCGTCCA ANCCGTAGTA GTGGTCATAG TCACCCAGCA GGCTCTGTCT      60
155 TTCGCACAAG TAAAAGACAG CCGTGTCCTC AGTTCTCAGC CTGTTCATTT TTAGATACAC     120
157 CGTGTTCTTG GAAGTGTCTC TGGAGATGGT GAATCGCCCC TTCACGGAGT CTGCGTAGTA     180
159 TTTAGTGCTT CCATCATATG ATATAACTGC CACCCACTCC AGCCCCTTGC CTAGAGCCTG     240
161 GCGGACCCAG TGCATAGCAA AGCTTCTGAA GGGGAATCCA GAGGCTGCAC AGGAGAGTCT     300
163 CAGGGACCTC CCAGGCTGGA CCACGCCTCC CCCAGACTCC ACCAGCTGCA CCTGACACTG     360
165 GATACCTCTT AAAAGAGCAA CGAGGAAAAC CCAGCTCAGC CCAAACTCCA TGGTGAGTCC     420
167 TCTGTGTTCA GTGATGAAGC TTGAAATCAC TAGTGCGGCC GCCTGCAGGT CGACCATATG     480
169 GGAGAGCTCC CAACGCGTTG GATGCATAGC TTGAGTATTC TATAGTGTCA CCTAAATAGC     540
171 TTG                                                                   543
173 (2) INFORMATION FOR SEQ ID NO: 4:
175      (i) SEQUENCE CHARACTERISTICS:
176              (A) LENGTH: 450 base pairs
177              (B) TYPE: nucleic acid
178              (C) STRANDEDNESS: double
179              (D) TOPOLOGY: linear
183      (ix) FEATURE:
184              (A) NAME/KEY: CDS
185              (B) LOCATION: 1..450
188      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
190 CTCGAGATGG ACATGGAGTT CCAGGCGCAG CTTCTCTTCC TCCTGCTACT CTGGCTCCCA      60
192 GATATCACCG GAGATATTGT GTTGACGCAG TCTCCAGGCA CCCTGTCTTT GTCTCCAGGG     120
194 GAAAGAGCCA CCCTCTCCTG CAGGGCCAGT CAGAGTGTTA GTAGCAGCTA CTTAGCCTGG     180
196 TACCAGCAGA AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATGGTGCATC CACCAGGGCC     240
198 ACTGGCATGC CAGACAGGTC CAGTGGCAGT GGGTCCGGGA CAGACTTCAC TCTCACCATC     300
200 AGTAGACTGG AGCCTGAAGA TTTTGCAGTG TATTACTGTC AGCAGTATGG TAGCTCACCT     360
202 CAGACACCTC AGATCACTTT CGGCGGAGGG ACCAAGGTGG AGATCAAACG AACTGTGGCT     420
204 GCACCATCTG TCTTCATCTT CCCGCCATCT                                      450
206 (2) INFORMATION FOR SEQ ID NO: 5:
208      (i) SEQUENCE CHARACTERISTICS:
209              (A) LENGTH: 150 amino acids
210              (B) TYPE: amino acid
211              (C) STRANDEDNESS: single
212              (D) TOPOLOGY: linear
218      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
220      Leu Glu Met Asp Met Glu Phe Gln Ala Gln Leu Leu Phe Leu Leu Leu
221      1               5                   10                  15
223      Leu Trp Leu Pro Asp Ile Thr Gly Asp Ile Val Leu Thr Gln Ser Pro
224                      20                  25                  30
226      Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
227              35                  40                  45
229      Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
230          50                  55                  60
232      Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala
233      65                  70                  75                  80
235      Thr Gly Met Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
236                      85                  90                  95
```

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```
238       Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
239               100                 105                 110
241       Cys Gln Gln Tyr Gly Ser Ser Pro Gln Thr Pro Gln Ile Thr Phe Gly
242               115                 120                 125
244       Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
245           130                 135                 140    :
247       Phe Ile Phe Pro Pro Ser
248       145                 150
250 (2) INFORMATION FOR SEQ ID NO: 6:
252       (i) SEQUENCE CHARACTERISTICS:
253           (A) LENGTH: 450 base pairs
254           (B) TYPE: nucleic acid
255           (C) STRANDEDNESS: double
256           (D) TOPOLOGY: linear
262       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
264 AGATGGCGGG AAGATGAAGA CAGATGGTGC AGCCACAGTT CGTTTGATCT CCACCTTGGT        60
266 CCCTCCGCCG AAAGTGATCT GAGGTGTCTG AGGTGAGCTA CCATACTGCT GACAGTAATA       120
268 CACTGCAAAA TCTTCAGGCT CCAGTCTACT GATGGTGAGA GTGAAGTCTG TCCCGGACCC       180
270 ACTGCCACTG AACCTGTCTG GCATGCCAGT GGCCCTGGTG GATGCACCAT AGATGAGGAG       240
272 CCTGGGAGCC TGGCCAGGTT TCTGCTGGTA CCAGGCTAAG TAGCTGCTAC TAACACTCTG       300
274 ACTGGCCCTG CAGGAGAGGG TGGCTCTTTC CCCTGGAGAC AAAGACAGGG TGCCTGGAGA       360
276 CTGCGTCAAC ACAATATCTC CGGTGATATC TGGGAGCCAG AGTAGCAGGA GGAAGAGAAG       420
278 CTGCGCCTGG AACTCCATGT CCATCTCGAG                                        450
280 (2) INFORMATION FOR SEQ ID NO: 7:
282       (i) SEQUENCE CHARACTERISTICS:
283           (A) LENGTH: 34 base pairs
284           (B) TYPE: nucleic acid
285           (C) STRANDEDNESS: single
286           (D) TOPOLOGY: linear
292       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
294 TATGAAGACA CCAGGCCGAT ATTGTGTTGA CGCA                                    34
296 (2) INFORMATION FOR SEQ ID NO: 8:
298       (i) SEQUENCE CHARACTERISTICS:
299           (A) LENGTH: 26 base pairs
300           (B) TYPE: nucleic acid
301           (C) STRANDEDNESS: single
302           (D) TOPOLOGY: linear
308       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
310 TATCCGGATG CAGCCACAGT TCGTTT                                             26
312 (2) INFORMATION FOR SEQ ID NO: 9:
314       (i) SEQUENCE CHARACTERISTICS:
315           (A) LENGTH: 26 base pairs
316           (B) TYPE: nucleic acid
317           (C) STRANDEDNESS: single
318           (D) TOPOLOGY: linear
324       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
326 TATTCGGACA GGTGCAGCTG GTGGAG                                             26
328 (2) INFORMATION FOR SEQ ID NO: 10:
330       (i) SEQUENCE CHARACTERISTICS:
```

```
331              (A) LENGTH: 27 base pairs
332              (B) TYPE: nucleic acid
333              (C) STRANDEDNESS: single
334              (D) TOPOLOGY: linear
340      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
342 TATGGATCCT GAGGAGACGG TGACCGT                                        27
344 (2) INFORMATION FOR SEQ ID NO: 11:
346      (i) SEQUENCE CHARACTERISTICS:
347              (A) LENGTH: 60 base pairs
348              (B) TYPE: nucleic acid
349              (C) STRANDEDNESS: single
350              (D) TOPOLOGY: linear
356      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
358 TATATATCCG GAGGTGGTGG ATCAGGTGGA GGTGGCTCCC AGGTGCAGCT GGTGGAGTCT    60
361 (2) INFORMATION FOR SEQ ID NO: 12:
363      (i) SEQUENCE CHARACTERISTICS:
364              (A) LENGTH: 46 base pairs
365              (B) TYPE: nucleic acid
366              (C) STRANDEDNESS: single
367              (D) TOPOLOGY: linear
373      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
375 ACCTCCGGAA CCGCCACCGC CAGAGACAGA TGGTGCAGCC ACATTC                   46
377 (2) INFORMATION FOR SEQ ID NO: 13:
379      (i) SEQUENCE CHARACTERISTICS:
380              (A) LENGTH: 918 base pairs
381              (B) TYPE: nucleic acid
382              (C) STRANDEDNESS: single
383              (D) TOPOLOGY: linear
387      (ix) FEATURE:
388              (A) NAME/KEY: CDS
389              (B) LOCATION: join(1..906, 913..918)
392      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
394 GAA TTC ATG AAA AAA ACC GCT ATC GCG ATC GCA GTT GCA CTG GCT GGT      48
395 Glu Phe Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly
396  1               5                   10                  15
398 TTC GCT ACC GTT GCG CAG GCC GAT ATT GTG TTG ACG CAG TCT CCA GGC      96
399 Phe Ala Thr Val Ala Gln Ala Asp Ile Val Leu Thr Gln Ser Pro Gly
400          20                  25                  30
402 ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC AGG GCC     144
403 Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
404          35                  40                  45
406 AGT CAG AGT GTT AGT AGC AGC TAC TTA GCC TGG TAC CAG CAG AAA CCT     192
407 Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
408      50                  55                  60
410 GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT GCA TCC ACC AGG GCC ACT     240
411 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
412  65                  70                  75                  80
414 GGC ATG CCA GAC AGG TTC AGT GGC AGT GGG TCC GGG ACA GAC TTC ACT     288
415 Gly Met Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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VERIFICATION SUMMARY   DATE: 09/15/2003
PATENT APPLICATION: **US/09/194,164**   TIME: 15:42:29

Input Set ·: **N:\Crf3\RULE60\09194164.RAW.txt**
Output Set: **N:\CRF4\09152003\I194164.raw**

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]